



INFORMATION DISCLOSURE STATEMENT BY APPLICANT (use as many sheets as necessary)			Complete if Known		
			Application Number	09/782,004	
			Filing Date	February 12, 2001	
			First Named Inventor	DAHIYAT, Bassil I.	
			Group Art Unit	1627	
			Examiner Name	WESSENDORF, Teresa D.	
Sheet	1	of	1	Attorney Docket Number	A-67229-6/RFT/RMS/RMK (463077-5)

U.S. PATENT DOCUMENTS					
Examiner Initials*	Cite No.	U.S. Patent Document Number-Kind Code ² (if known)	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
<i>MB</i>	A1	5,265,030	11-23-1993	Skolnick et al.	
<i>MB</i>	A2	5,878,373	03-02-1999	Cohen et al.	
	A3				
	A4				
	A5				
	A6				
	A7				
	A8				
	A9				
	A10				

FOREIGN PATENT DOCUMENTS						
Examiner Initials*	Cite No.	Foreign Patent Document Country Code ² Number ² Kind Code ² (if known)	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T ⁴
	B1					
	B2					
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<i>MB</i>	C1	Fechteler T, et al., "Prediction of protein three-dimensional structures in insertion and deletion regions: a procedure for searching data bases of representative protein fragments using geometric scoring criteria." J Mol Biol. 1995 Oct 13;253(1):114-31.		
<i>MB</i>	C2	Malakauskas SM, and Mayo SL. "Design, structure and stability of a hyperthermophilic protein variant." Nat Struct Biol. 1998 Jun;5(6):470-5.		
<i>MB</i>	C3	Wallace AC, et al., "Derivation of 3D coordinate templates for searching structural databases: application to Ser-His-Asp catalytic triads in the serine proteinases and lipases." Protin Sci. 1996 Jun;5(6):1001-13.		
<i>MB</i>	C4			
	C5			

Examiner Signature	<i>[Signature]</i>	Date Considered	11/04
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INFORMATION DISCLOSURE STATEMENT BY APPLICANT

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Sheet 1 of 4 Application Number 09/782,004 Filing Date February 12, 2001 First Named Inventor Bassil I. Dahiyat Group Art Unit 1645 Examiner Name not yet assigned Attorney Docket Number A-67229-6/RFT/RMS/RMK

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		Number	Kind Code ² (if known)			
MM	A1	4,939,666		Hardman, K.D.	07/03/1990	
	A2	5,241,470		Lee et al.	08/31/1993	
	A3	6,188,965		Mayo et al.	02/13/2001	
MM	A4	6,269,312		Mayo et al.	07/31/2001	

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		Office ³	Number ⁴ (if known)	Kind Code ² (if known)				
MM	B1	WO	98/47089	A1	CALIFORNIA INSTITUTE OF TECHNOLOGY	10/22/1998		

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MM	C1	Brenner and Berry, A., et al., "A quantitative methodology for the de novo design of proteins", Protein Sci. 3:1871-1882 (Oct. 1994).	
	C2	Borman, "Proteins to Order," Chemical and Engineering Newsletter (C&EN) Oct. 6, 1997, 9-10 (1997).	
	C3	Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science vol. 247:1306-1310 (Mar. 1990).	
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	C5	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science vol.221(4612):709-713 (Aug. 1983).	
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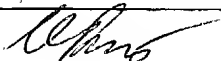
Complete If Known

Application Number	09/782,004
Filing Date	February 12, 2001
First Named Inventor	Bassil I. Dahiyat
Group Art Unit	1645
Examiner Name	not yet assigned
Attorney Docket Number	A-67229-6/RFT/RMS/RMK

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ms	C7	Dahiyat, B.I., et al., "Automated design of the surface positions of protein helices", Protein Science 6:1333-1337 (Jun. 1997).	
	C8	Dahiyat et al., "Protein design automation," Caltech Biology Annual Report, 172 (1995).	
	C9	Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science vol. 4, Suppl. 2, 83 (1995).	
	C10	Dahiyat et al., "Protein Design Automation," Poster Sessions, Protein Science vol. 5, Suppl. 1, 22-23 (1996).	
	C11	Dahiyat et al., "Probing the Role of Specificity in Protein Design," Caltech Biology Annual Report, 160-161 (1996).	
	C12	Dahiyat, B.I., et al., "First fully automatic design of a protein achieved by Caltech scientists", new press release (Oct. 1997).	
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	C14	DeGrado, W., "Proteins from Scratch," Science, 278:80-81 (1997).	
	C15	Desjarlais et al., "New strategies in protein design," Current Opinion in Biotechnology :460-466 (1995).	
	C16	Desmet, J., et al., "The 'Dead End Elimination' Theorem: A New Approach to the Side Chain Packing Protein", from "The Protein Folding Problem and Tertiary Structure Prediction" Ch.10:1-49 (1994).	
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	C19	Dunbrack Jr., R.L., et al., "Conformational analysis of the backbone-dependent rotamer preferences of protein sidechains", Struc. Biol. vol.1(5):334-340 (May 1994).	
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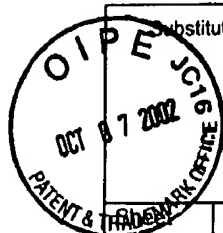
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mm	C22	Gordon et al. "Energy functions for protein design," Curr. Opinion in Struct. Biol., 9:509-513 (1999).	
	C23	Harbury et al., "High-Resolution Protein Design with Backbone Freedom," Science, 282:1462-1467 (1998).	
	C24	Hellings, H.W., et al., "Construction of New Ligand Binding Site in Proteins of Known Structure", J. Mol. Biol. 222:763-785 (1991).	
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	C27	Hurley et al., "Design and Structural Analysis of Alternative Hydrophobic Core Packing Arrangements in Bacteriophage T4 Lysozyme," J. Mol. Biol., 224:1143-1159(1992).	
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